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Sequence Listing could not be accepted due to errors.  
See attached Validation Report.  
If you need help call the Patent Electronic Business Center at (866)  
217-9197 (toll free).  
Reviewer: markspencer  
Timestamp: [year=2008; month=9; day=22; hr=9; min=26; sec=4; ms=670; ]  
=====

\*\*\*\*\*

Reviewer Comments:

<110> The University of Newcastle

Connolly, Bernard

Fogg, Mark

Pearl, Laurence

<120> DNA POLYMERASES  
<130> P89103PWO  
<140> 105111130  
<141> 2005-08-15  
<150> PCT/GB2003/001623  
<151> 2003-04-15  
<160> 32

Numeric identifier <160> must reflect the total number of sequences found in the sequence listing. This file contains 33 SEQ ID numbers, but <160> states there are 32. Please make all necessary changes.

<210> 13  
<211> 103  
<212> PRT  
<213> RB69

\* \* \* \* \*

Numeric identifier <213> can only be one of three choices, "Scientific name, i.e. Genus/species, Unknown or Artificial Sequence." Please make all necessary changes.

<210> 33  
<211> 13  
<212> PRT  
<213> Unknown  
<220>  
<223> amino acid motif where X can be any amino acid  
  
<400> 33

Glu Xaa Xaa Ile Xaa Phe/Tyr Xaa Xaa Xaa Tyr Xaa Xaa Asp  
1          5     10

Numeric identifier <211> must reflect the total number of amino acids in the sequence. <211> states there are 13 amino acids in SEQ ID # 33, but the actual count is 14. Please make all necessary changes.

A sequence cannot contain any non-sequence related symbols. Please remove "/" from SEQ ID # 33.

\*\*\*\*\*

Application No: 10511130

Version No: 2.0

Input Set:

Output Set:

Started: 2008-09-20 06:22:41.144

Finished: 2008-09-20 06:22:44.841

Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 697 ms

Total Warnings: 23

Total Errors: 2

No. of SeqIDs Defined: 32

Actual SeqID Count: 33

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 402	Undefined organism found in <213> in SEQ ID (12)
W 402	Undefined organism found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 402	Undefined organism found in <213> in SEQ ID (19)
W 402	Undefined organism found in <213> in SEQ ID (20)
W 402	Undefined organism found in <213> in SEQ ID (21)
W 402	Undefined organism found in <213> in SEQ ID (22)

**Input Set:**

**Output Set:**

**Started:** 2008-09-20 06:22:41.144  
**Finished:** 2008-09-20 06:22:44.841  
**Elapsed:** 0 hr(s) 0 min(s) 3 sec(s) 697 ms  
**Total Warnings:** 23  
**Total Errors:** 2  
**No. of SeqIDs Defined:** 32  
**Actual SeqID Count:** 33

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (29)
W 213	Artificial or Unknown found in <213> in SEQ ID (33)
E 330	Invalid protein , found in SEQID(33) POS (6)Invalid
W 333	tabs used in amino acid numbering SEQID (33)
E 252	Calc# of Seq. differs from actual; 32 seqIds defined; count=33

# SEQUENCE LISTING

<110> The University of Newcastle

Connolly, Bernard

Fogg, Mark

Pearl, Laurence

<120> DNA POLYMERASES

<130> P89103FWO

<140> 10511130

<141> 2005-08-15

<150> PCT/GB2003/001623

<151> 2003-04-15

<160> 32

<170> PatentIn version 3.1

<210> 1

<211> 776

<212> PRT

<213> Unknown

<220>

<223> Variant derived from Pyrococcus furiosus Pfu-Polymerase

<400> 1

Met Ala Ile Leu Asp Val Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val

1

5

10

15

Ile Arg Leu Phe Lys Lys Glu Asn Gly Lys Phe Lys Ile Glu His Asp  
20 25 30

Arg Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys  
35 40 45

Ile Glu Glu Val Lys Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val  
50 55 60

Arg Ile Val Asp Val Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro  
65 70 75 80

Ile Thr Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr  
85 90 95

Ile Arg Glu Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu  
100 105 110

Tyr Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile  
115 120 125

Pro Met Glu Gly Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu  
130 135 140

Thr Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met  
145 150 155 160

Ile Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn  
165 170 175

Ile Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile  
180 185 190

Lys Arg Phe Leu Arg Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Val  
195 200 205

Thr Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala  
210 215 220

Glu Lys Leu Gly Ile Lys Leu Thr Ile Gly Arg Asp Gly Ser Glu Pro  
225 230 235 240

Lys Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg  
 245 250 255

Ile His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro  
 260 265 270

Thr Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys  
 275 280 285

Glu Lys Val Tyr Ala Asp Glu Ile Ala Lys Ala Trp Glu Ser Gly Glu  
 290 295 300

Asn Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr  
 305 310 315 320

Tyr Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg  
 325 330 335

Leu Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn  
 340 345 350

Leu Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val  
 355 360 365

Ala Pro Asn Lys Pro Ser Glu Glu Glu Tyr Gln Arg Arg Leu Arg Glu  
 370 375 380

Ser Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu  
 385 390 395 400

Asn Ile Val Tyr Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile  
 405 410 415

Thr His Asn Val Ser Pro Asp Thr Leu Asn Leu Glu Gly Cys Lys Asn  
 420 425 430

Tyr Asp Ile Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Ile Pro  
 435 440 445

Gly Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Lys  
 450 455 460

Ile Lys Thr Lys Met Lys Glu Thr Gln Asp Pro Ile Glu Lys Ile Leu  
465 470 475 480

Leu Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr  
485 490 495

Gly Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala  
500 505 510

Glu Ser Val Thr Ala Trp Gly Arg Lys Tyr Ile Glu Leu Val Trp Lys  
515 520 525

Glu Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp  
530 535 540

Gly Leu Tyr Ala Thr Ile Pro Gly Gly Glu Ser Glu Glu Ile Lys Lys  
545 550 555 560

Lys Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu  
565 570 575

Leu Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr  
580 585 590

Lys Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Val Ile Thr Arg  
595 600 605

Gly Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr  
610 615 620

Gln Ala Arg Val Leu Glu Thr Ile Leu Lys His Gly Asp Val Glu Glu  
625 630 635 640

Ala Val Arg Ile Val Lys Glu Val Ile Gln Lys Leu Ala Asn Tyr Glu  
645 650 655

Ile Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu  
660 665 670

His Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu  
675 680 685

Ala Ala Lys Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile



690

695

700

Val Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu  
 705 710 715 720

Glu Tyr Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu  
 725 730 735

Asn Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr  
 740 745 750

Arg Lys Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Thr  
 755 760 765

Ser Trp Leu Asn Ile Lys Lys Ser  
 770 775

&lt;210&gt; 2

&lt;211&gt; 775

&lt;212&gt; PRT

<213> *Pyrococcus furiosus*

&lt;400&gt; 2

Met Ile Leu Asp Val Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile  
 1 5 10 15

Arg Leu Phe Lys Lys Glu Asn Gly Lys Phe Lys Ile Glu His Asp Arg  
 20 25 30

Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys Ile  
 35 40 45

Glu Glu Val Lys Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg  
 50 55 60

Ile Val Asp Val Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro Ile  
 65 70 75 80

Thr Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr Ile  
 85 90 95

Arg Glu Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr  
100 105 110

Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro  
115 120 125

Met Glu Gly Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr  
130 135 140

Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile  
145 150 155 160

Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn Ile  
165 170 175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys  
180 185 190

Arg Phe Leu Arg Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Val Thr  
195 200 205

Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu  
210 215 220

Lys Leu Gly Ile Lys Leu Thr Ile Gly Arg Asp Gly Ser Glu Pro Lys  
225 230 235 240

Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile  
245 250 255

His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro Thr  
260 265 270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu  
275 280 285

Lys Val Tyr Ala Asp Glu Ile Ala Lys Ala Trp Glu Ser Gly Glu Asn  
290 295 300

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr  
305 310 315 320

Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu  
 325 330 335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu  
 340 345 350

Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala  
 355 360 365

Pro Asn Lys Pro Ser Glu Glu Glu Tyr Gln Arg Arg Leu Arg Glu Ser  
 370 375 380

Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn  
 385 390 395 400

Ile Val Tyr Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr  
 405 410 415

His Asn Val Ser Pro Asp Thr Leu Asn Leu Glu Gly Cys Lys Asn Tyr  
 420 425 430

Asp Ile Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Ile Pro Gly  
 435 440 445

Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Lys Ile  
 450 455 460

Lys Thr Lys Met Lys Glu Thr Gln Asp Pro Ile Glu Lys Ile Leu Leu  
 465 470 475 480

Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr Gly  
 485 490 495

Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu  
 500 505 510

Ser Val Thr Ala Trp Gly Arg Lys Tyr Ile Glu Leu Val Trp Lys Glu  
 515 520 525

Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly  
 530 535 540

Leu Tyr Ala Thr Ile Pro Gly Gly Glu Ser Glu Glu Ile Lys Lys Lys  
545 550 555 560

Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu  
565 570 575

Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys  
580 585 590

Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Val Ile Thr Arg Gly  
595 600 605

Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln  
610 615 620

Ala Arg Val Leu Glu Thr Ile Leu Lys His Gly Asp Val Glu Glu Ala  
625 630 635 640

Val Arg Ile Val Lys Glu Val Ile Gln Lys Leu Ala Asn Tyr Glu Ile  
645 650 655

Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His  
660 665 670

Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala  
675 680 685

Ala Lys Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val  
690 695 700

Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu  
705 710 715 720

Tyr Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn  
725 730 735

Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg  
740 745 750

Lys Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Thr Ser  
755 760 765

Trp Leu Asn Ile Lys Lys Ser

&lt;210&gt; 3

&lt;211&gt; 776

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

<223> Variant derived from *Pyrococcus furiosus* Pfu-Polymerase

&lt;400&gt; 3

Met Ala Ile Leu Asp Val Asp Ala Ile Thr Glu Glu Gly Lys Pro Val  
 1 5 10 15

Ile Arg Leu Phe Lys Lys Glu Asn Gly Lys Phe Lys Ile Glu His Asp  
 20 25 30

Arg Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys  
 35 40 45

Ile Glu Glu Val Lys Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val  
 50 55 60

Arg Ile Val Asp Val Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro  
 65 70 75 80

Ile Thr Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr  
 85 90 95

Ile Arg Glu Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu  
 100 105 110

Tyr Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile  
 115 120 125

Pro Met Glu Gly Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu  
 130 135 140

Thr Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met  
 145 150 155 160

Ile Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn  
165 170 175

Ile Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile  
180 185 190

Lys Arg Phe Leu Arg Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Val  
195 200 205

Thr Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala  
210 215 220

Glu Lys Leu Gly Ile Lys Leu Thr Ile Gly Arg Asp Gly Ser Glu Pro  
225 230 235 240

Lys Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg  
245 250 255

Ile His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro  
260 265 270

Thr Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys  
275 280 285

Glu Lys Val Tyr Ala Asp Glu Ile Ala Lys Ala Trp Glu Ser Gly Glu  
290 295 300

Asn Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr  
305 310 315 320

Tyr Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg  
325 330 335

Leu Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn  
340 345 350

Leu Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val  
355 360 365

Ala Pro Asn Lys Pro Ser Glu Glu Glu Tyr Gln Arg Arg Leu Arg Glu  
370 375 380

Ser Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu  
385 390 395 400

Asn Ile Val Tyr Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile  
405 410 415

Thr His Asn Val Ser Pro Asp Thr Leu Asn Leu Glu Gly Cys Lys Asn  
420 425 430

Tyr Asp Ile Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Ile Pro  
435 440 445

Gly Phe Ile Pro Ser Leu Leu Gly His Leu L